

Fig. 1

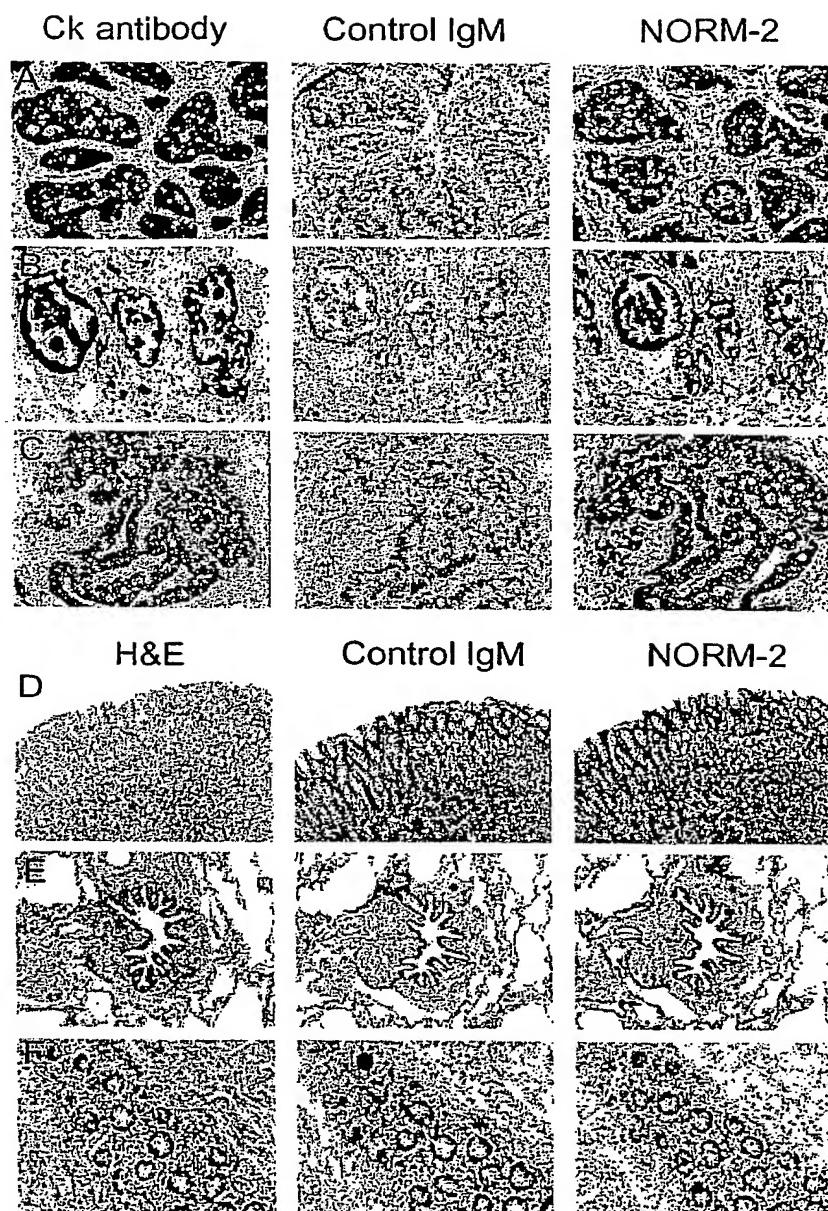


Fig. 2

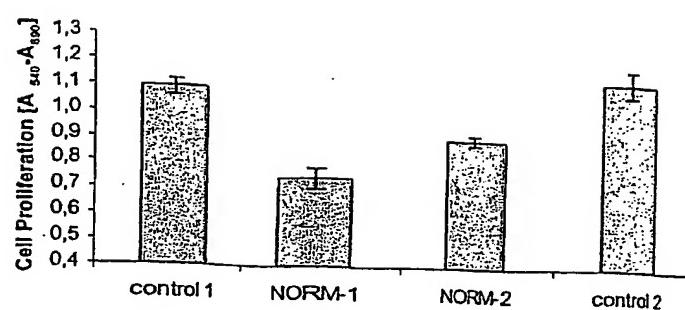


Fig. 3

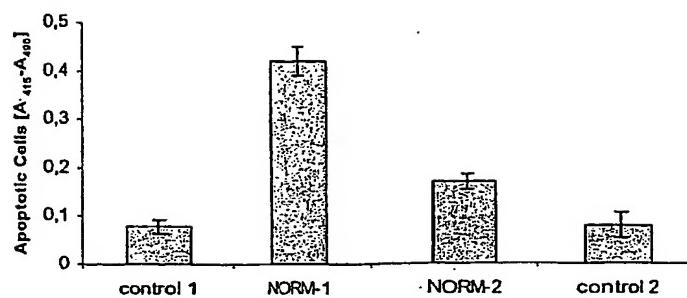


Fig. 4

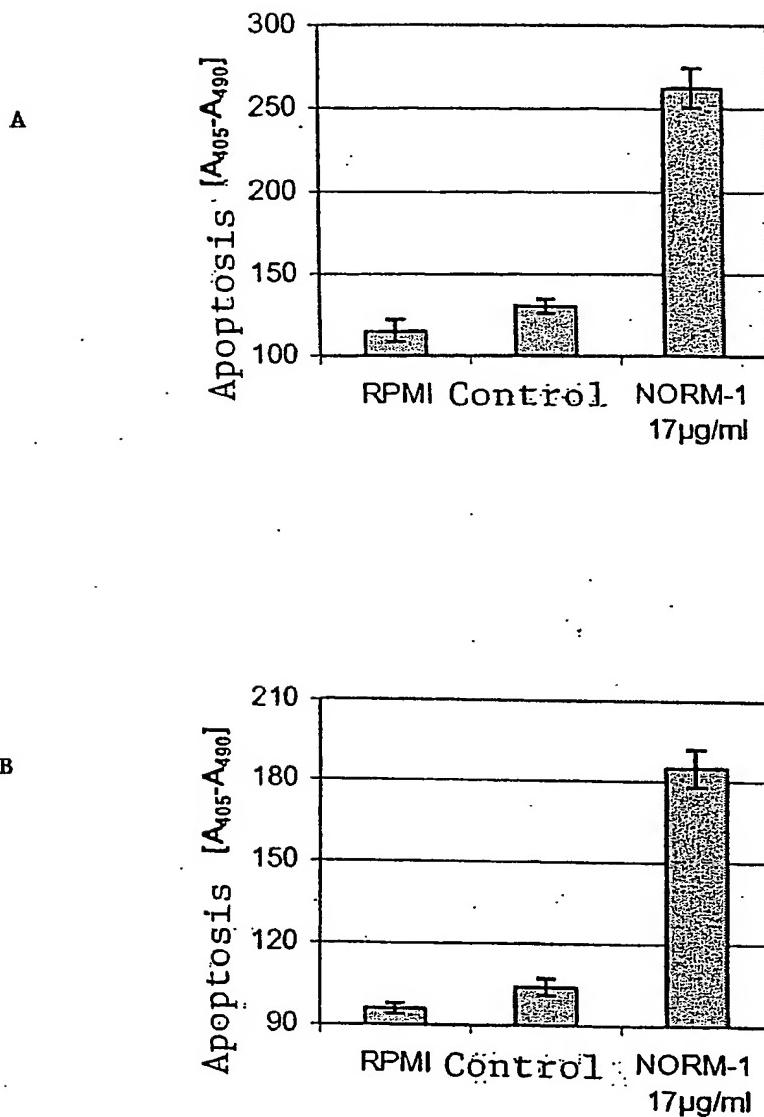


Fig. 5

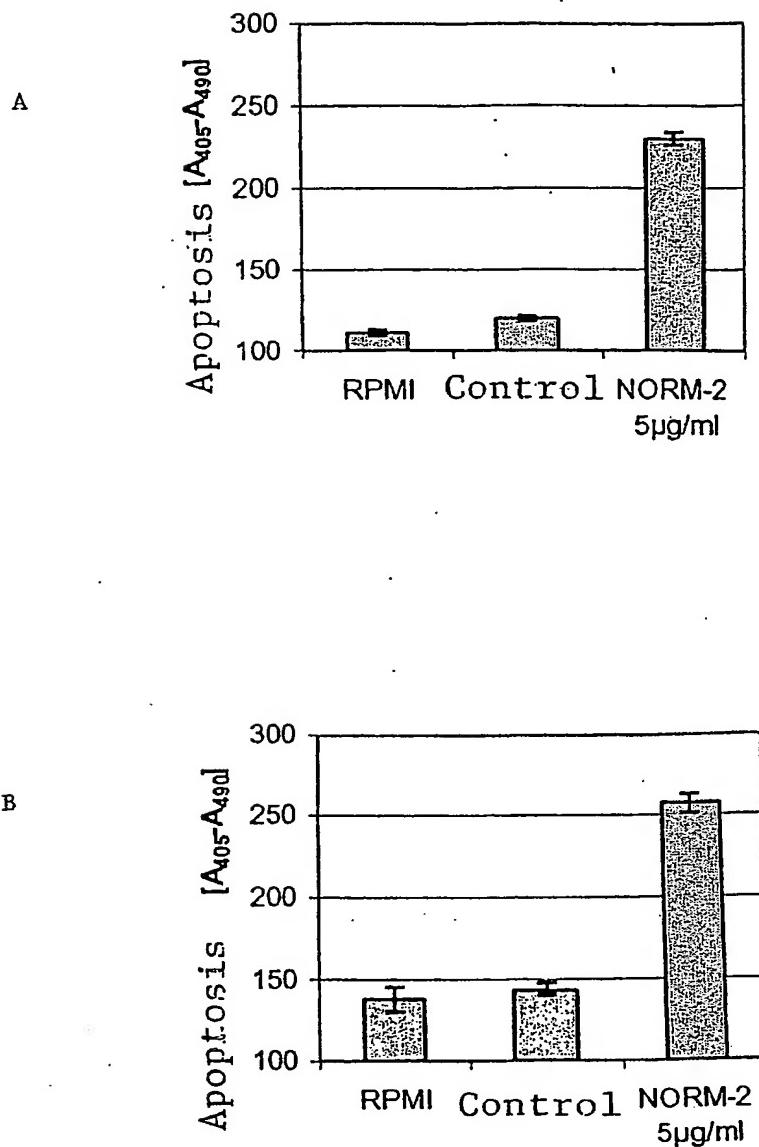


Fig. 6

NORM-1 (VH)

CDR3		D-Region		J-Region	
1	10	105	105		
5	15	91	91		
10	20	148	148		
15	25	30	30	CDR2	
20	30	35	35		
25	35	40	40		
30	40	45	45		
35	45	50	50		
40	50	55	55		
45	55	60	60		
50	60	65	65		
55	65	70	70		
60	70	75	75		
65	75	80	80		
70	80	85	85		
75	85	90	90		
80	90	95	95		
85	95	100	100		
90	100	105	105		
95	105	110	110		
100	110	115	115		
105	115	120	120		
110	120	125	125		
115	125	130	130		
120	130	135	135		
125	135	140	140		
130	140	145	145		
135	145	150	150		
140	150	155	155		
145	155	160	160		
150	160	165	165		
155	165	170	170		
160	170	175	175		
165	175	180	180		
170	180	185	185		
175	185	190	190		
180	190	195	195		
185	195	200	200		
190	200	205	205		
195	205	210	210		
200	210	215	215		
205	215	220	220		
210	220	225	225		
215	225	230	230		
220	230	235	235		
225	235	240	240		
230	240	245	245		
235	245	250	250		
240	250	255	255		
245	255	260	260		
250	260	265	265		
255	265	270	270		
260	270	275	275		
265	275	280	280		
270	280	285	285		
275	285	290	290		
280	290	295	295		
285	295	300	300		
290	300	305	305		
295	305	310	310		
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305	315	320	320		
310	320	325	325		
315	325	330	330		
320	330	335	335		
325	335	340	340		
330	340	345	345		
335	345	350	350		
340	350	355	355		
345	355	360	360		
350	360	365	365		
355	365	370	370		
360	370	375	375		
365	375	380	380		
370	380	385	385		
375	385	390	390		
380	390	395	395		
385	395	400	400		
390	400	405	405		
395	405	410	410		
400	410	415	415		
405	415	420	420		
410	420	425	425		
415	425	430	430		
420	430	435	435		
425	435	440	440		
430	440	445	445		
435	445	450	450		
440	450	455	455		
445	455	460	460		
450	460	465	465		
455	465	470	470		
460	470	475	475		
465	475	480	480		
470	480	485	485		
475	485	490	490		
480	490	495	495		
485	495	500	500		
490	500	505	505		
495	505	510	510		
500	510	515	515		
505	515	520	520		
510	520	525	525		
515	525	530	530		
520	530	535	535		
525	535	540	540		
530	540	545	545		
535	545	550	550		
540	550	555	555		
545	555	560	560		
550	560	565	565		
555	565	570	570		
560	570	575	575		
565	575	580	580		
570	580	585	585		
575	585	590	590		
580	590	595	595		
585	595	600	600		
590	600	605	605		
595	605	610	610		
600	610	615	615		
605	615	620	620		
610	620	625	625		
615	625	630	630		
620	630	635	635		
625	635	640	640		
630	640	645	645		
635	645	650	650		
640	650	655	655		
645	655	660	660		
650	660	665	665		
655	665	670	670		
660	670	675	675		
665	675	680	680		
670	680	685	685		
675	685	690	690		
680	690	695	695		
685	695	700	700		
690	700	705	705		
695	705	710	710		
700	710	715	715		
705	715	720	720		
710	720	725	725		
715	725	730	730		
720	730	735	735		
725	735	740	740		
730	740	745	745		
735	745	750	750		
740	750	755	755		
745	755	760	760		
750	760	765	765		
755	765	770	770		
760	770	775	775		
765	775	780	780		
770	780	785	785		
775	785	790	790		
780	790	795	795		
785	795	800	800		
790	800	805	805		
795	805	810	810		
800	810	815	815		
805	815	820	820		
810	820	825	825		
815	825	830	830		
820	830	835	835		
825	835	840	840		
830	840	845	845		
835	845	850	850		
840	850	855	855		
845	855	860	860		
850	860	865	865		
855	865	870	870		
860	870	875	875		
865	875	880	880		
870	880	885	885		
875	885	890	890		
880	890	895	895		
885	895	900	900		
890	900	905	905		
895	905	910	910		
900	910	915	915		
905	915	920	920		
910	920	925	925		
915	925	930	930		
920	930	935	935		
925	935	940	940		
930	940	945	945		
935	945	950	950		
940	950	955	955		
945	955	960	960		
950	960	965	965		
955	965	970	970		
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965	975	980	980		
970	980	985	985		
975	985	990	990		
980	990	995	995		
985	995	1000	1000		
990	1000	1005	1005		
995	1005	1010	1010		
1000	1010	1015	1015		
1005	1015	1020	1020		
1010	1020	1025	1025		
1015	1025	1030	1030		
1020	1030	1035	1035		
1025	1035	1040	1040		
1030	1040	1045	1045		
1035	1045	1050	1050		
1040	1050	1055	1055		
1045	1055	1060	1060		
1050	1060	1065	1065		
1055	1065	1070	1070		
1060	1070	1075	1075		
1065	1075	1080	1080		
1070	1080	1085	1085		
1075	1085	1090	1090		
1080	1090	1095	1095		
1085	1095	1100	1100		
1090	1100	1105	1105		
1095	1105	1110	1110		
1100	1110	1115	1115		
1105	1115	1120	1120		
1110	1120	1125	1125		
1115	1125	1130	1130		
1120	1130	1135	1135		
1125	1135	1140	1140		
1130	1140	1145	1145		
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1165	1175	1180	1180		
1170	1180	1185	1185		
1175	1185	1190	1190		
1180	1190	1195	1195		
1185	1195	1200	1200		
1190	1200	1205	1205		
1195	1205	1210	1210		
1200	1210	1215	1215		
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1275	1285	1290	1290		
1280	1290	1295	1295		
1285	1295	1300	1300		
1290	1300	1305	1305		
1295	1305	1310	1310		
1300	1310	1315	1315		
1305	1315	1320	1320		
1310	1320	1325	1325		
1315	1325	1330	1330		
1320	1330	1335	1335		
1325	1335	1340	1340		
1330	1340	1345	1345		
1335	1345	1350	1350		
1340	1350	1355	1355		

Fig. 7

NORM-1 (VL)

TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile
1 5 10 15 20 60

CDR1 67 99 120

ACC TGC TCT GGA GAT GCA TTG CCA AAA TAT GCT TAT TGG TAC CAG CAG AAG TCA GGC
Thr Cys Ser Gly Asp Ala Leu Pro Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly
25 30 35 40 180

CDR2 145 165 180

CAG GCC CCT GTG CTG GTC ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
45 50 55 60

J-Region 240

TTC TCT GGC TCC AGC TCA GGG ACA ATG GCC ACC TTG ACT ATC AGT GGT GGC CAG GTG GAG
Phe Ser Gly Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
65 70 75 80 240

CDR3 262 297 300

GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTG TTC (SEQ. ID. NO: 4)
Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Ser Thr Asp Ser Ser Gly Asn His Ser Tyr Val Phe (SEQ. ID. NO: 3)
85 90 95 100 300

NORM-2 (VH)

GAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGG	CTG	GTC	AAG	CCT	GGG	TCC	CTG	AGA	CTC	60	
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Leu	Vai	Lys	Pro	Gly	Gly	Ser	Leu	Arg	Leu	
1																		20	
																		15	
																		10	
																		5	
																		1	
CDR1																			
																		91	
																		105	
																		120	
TCC	TGT	GCA	GCC	TCT	GGG	TTC	ACC	TTC	AGT	AGC	TAT	ATG	AAC	TGG	GTC	CGC	CAG	GCT	120
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ser	Met	Asn	Trp	Val	Arg	Gln	Ala
																		40	
																		35	
																		30	
CDR2																			
																		148	
																		180	
CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCA	TCC	ATT	AGT	AGT	TAC	ATA	TAC	TAC	TAC	TAC	180
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Vai	Ser	Ser	Ser	Ile	Ser	Ser	Ser	Tyr	Ile	Tyr	Tyr	
																		60	
																		55	
																		50	
																		45	
CDR3																			
																		198	
																		198	
GCA	GAC	TCA	GTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	TCA	CTG	240
Ala	Asp	Ser	Vai	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
																		80	
																		70	
																		65	
J-Region																			
																		324	
																		324	
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	CAT	GGG	300
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	His	Gly
																		100	
																		95	
																		85	
																		80	
																		75	
																		70	
																		65	
																		60	
																		55	
																		50	
																		45	
																		40	
																		35	
																		30	
																		25	
																		20	
																		15	
																		10	
																		5	
																		1	

NORM-2 (VL)

CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG GTC ACC ATC
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile
1 5 10 15 20

67 108
CDR1

TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA GGT TAT GAT GTA CAC TGG TAC CAG CAG
Ser Cys Thr Gly Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln
25 30 35 40

154 174
CDR2

CTT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GRC
Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr Asn Ser Asn Arg Pro Ser Gly Val
45 50 55 60

240

CCT GAC CGG TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT GGG CTC
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

J-Region

271 300
CDR3

CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Ser Leu Ser Ala Leu
85 90 95 100

303

GTA TTC (SEQ. ID. NO: 8)
Val Phe (SEQ. ID. NO: 7)

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